IN THE CLAIMS:

Claims 1, 3 and 5 are amended herein. Claim 9 is withdrawn. New Claims 10 through 21 are added. All claims currently pending and under consideration in the referenced application are shown below in the Listing of Claims, which replaces all prior versions and listings of claims in the application. Applicants request that these claims be entered as amended.

Listing of Claims:

1. (Currently Amended) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting a set of three or more alignment points for each data trace, said alignment points being selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers, and ~~an~~ one or more internal peaks associated with internal bases that are highly conserved in the target nucleic acid, and assigning to said alignment points ~~each having~~ a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) assigning a sequence position number to each peak in each of the plurality of data traces~~, and sequence position numbers being assigned to~~ that maximizes the number of times that the sequence position number and the ~~matching~~ reference position number are assigned to a base of the same type; and

(c) aligning the data traces based on the assigned sequence position numbers.

2. (Original) The method of claim 1, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

3. (Currently Amended) The method of claim [2] 1, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

4. (Original) The method of claim 1, wherein four data traces, one for each nucleotide base type, are aligned.

5. (Currently Amended) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting a set of five or more alignment points for each data trace, said alignment points being selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers, and ~~an~~ one or more internal peaks associated with internal bases that are highly conserved in the target nucleic acid, and assigning to said alignment points ~~each having~~ a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) assigning a sequence position number to each peak in each of the plurality of data traces~~, and sequence position numbers being assigned to~~ that maximizes the number of times that the sequence position number and the ~~matching~~ reference position number are assigned to a base of the same type; and

(c) aligning the data traces based on the assigned sequence position numbers.

6. (Original) The method of claim 5, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

7. (Original) The method of claim 5, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

8. (Original) The method of claim 5, wherein four data traces, one for each nucleotide base type, are aligned.

9. (Withdrawn)

10. (New) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting for each data trace one or more alignment points corresponding to an internal peak associated with internal bases that are highly conserved in the target nucleic acid, and assigning to each alignment point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) assigning a sequence position number to each peak in each of the plurality of data traces that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type; and

(c) aligning the data traces based on the assigned sequence position numbers.

11. (New) The method of claim 1, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

12. (New) The method of claim 1, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

13. (New) The method of claim 1, wherein four data traces, one for each nucleotide base type, are aligned.

14. (New) The method of claim 10, further comprising alignment points selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers.

15. (New) The method of claim 14, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

16. (New) The method of claim 14, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

17. (New) The method of claim 14, wherein four data traces, one for each nucleotide base type, are aligned.

18. (New) The method of claim 1, further comprising the steps of determining the average peak spacing interval between alignment points and assigning sequence position numbers to peaks occurring at said intervals, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

19. (New) The method of claim 5, further comprising the steps of determining the average peak spacing interval between alignment points and assigning a sequence position number to peaks occurring at the intervals, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

20. (New) The method of claim 10, further comprising the steps of determining the average peak spacing interval between alignment points and assigning a sequence position number to peaks occurring at the intervals, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

21. (New) The method of claim 14, further comprising the steps of determining the average peak spacing interval between alignment points and assigning a sequence position number to peaks occurring at the intervals, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

IN THE TITLE:

Amend the Title of the present application as follows:

"Method ~~and Apparatus~~ for Alignment of DNA Sequencing Data Traces"

IN THE ABSTRACT:

Delete the Abstract of the Invention and replace with the following (a replacement page with the new Abstract is enclosed):

The present invention is directed to a method for alignment of nucleic acid data traces. The method involves selecting reference alignment points from among internal peaks representing highly conserved bases, preferably consisting of heterogeneous multiplets. The alignment points may also optionally include the primer peak and/or the full-length peak. Reference position numbers are assigned to these alignment points reflecting the known relative position of the alignment point, a sequence position number is assigned to peaks in the data traces so as to maximize assigning the sequence position number and the reference position number to the same base. Optionally, the method may include the step of determining the average peak spacing interval between alignment points and assigning a sequence position number to peaks occurring at the intervals. The data traces are then aligned based on the assigned sequence position numbers.